



SEQUENCE LISTING

<110> Ruoho, Arnold E.

Geiser, Andrew H.

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Sievert, Mike

<120> BACTERIORHODOPSIN/G PROTEIN-COUPLED RECEPTOR CHIMERAS

<130> 96429/9079

<140> US/09/389,835

<141> 1999-09-03

<150> 60/098,950

<151> 1998-09-03

a!
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<170> Word 97 (DOS text file)

<210> 1

<211> 1626

<212> DNA

<213> Halobacterium salinarium

<220>

<221> CDS

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cacgagtttt tcgtgcgctt cgagtggtaa cacgcgtgca cgcacgact tcaccgcggg 180

tgtttcgacg ccagccggcc gttgaaccag caggcagcgg gcatttcaca gccgctgtgg 240

cccacacact cgggtggggtg cgctattttg gtatggtttg gaatccgcgt gtcggctccg 300

tgtctgacgg ttcacgggtc taaattccgt cacgagcgta ccatactgat tgggtcgtag 360

agttacacac atatcctcgt taggtactgt tgc atg ttg gag tta ttg cca aca 414

Met Leu Glu Leu Leu Pro Thr

1

5

gca gtg gag ggg gta tcg cag gcc cag atc acc gga cgt ccg gag tgg 462

Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly Arg Pro Glu Trp

10

15

20

atc tgg cta gcg ctc ggt acg gcg cta atg gga ctc ggg acg ctc tat 510

Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu Gly Thr Leu Tyr

25

30

35

ttc ctc gtg aaa ggg atg ggc gtc tcg gac cca gat gca aag aaa ttc 558

Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp Ala Lys Lys Phe

40

45

50

55

tac gcc atc acg acg ctc gtc cca gcc atc gcg ttc acg atg tac ctc 606

Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe Thr Met Tyr Leu

60

65

70

tcg atg ctg ctg ggg tat ggc ctc aca atg gta ccg ttc ggt ggg gag 654

Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro Phe Gly Gly Glu

75

80

85

cag aac ccc atc tac tgg gcg cgg tac gct gac tgg ctg ttc acc acg 702

Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp Leu Phe Thr Thr

90

95

100

ccg ctg ttg ttg tta gac ctc gcg ttg ctc gtt gac gcg gat cag gga 750

Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp Ala Asp Gln Gly

105

110

115

acg atc ctt gcg ctc gtc ggt gcc gac ggc atc atg atc ggg acc ggc 798

Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met Ile Gly Thr Gly

120

125

130

135

ctg gtc ggc gca ctg acg aag gtc tac tcg tac cgc ttc gtg tgg tgg 846

Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg Phe Val Trp Trp

140

145

150

gcg atc agc acc gca gcg atg ctg tac atc ctg tac gtg ctg ttc ttc 894

Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr Val Leu Phe Phe

155

160

165

ggg ttc acc tcg aag gcc gaa agc atg cgc ccc gag gtc gca tcc acg 942

Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu Val Ala Ser Thr

170

175

180

ttc aaa gta ctg cgt aac gtt acc gtt gtg ttg tgg tcc gcg tat ccc 990
 Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp Ser Ala Tyr Pro
 185 190 195

gtc gtg tgg ctg atc ggc agc gaa ggt gcg gga atc gtg ccg ctg aac 1038
 Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile Val Pro Leu Asn
 200 205 210 215

atc gag acg ctg ctg ttc atg gtg ctt gac gtg agc gcg aag gtc ggc 1086
 Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser Ala Lys Val Gly
 220 225 230

ttc ggg ctc atc ctc ctg cgc agt cgt gcg atc ttc ggc gaa gcc gaa 1134
 Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe Gly Glu Ala Glu
 235 240 245

gcg ccg gag ccg tcc gcc ggc gac ggc gcg gcc gcg acc agc gac tga 1182
 Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala Thr Ser Asp
 250 255 260

tgcacacgc aggacagccc cacaaccggc gcggttttc aacgacacac gatgagtccc 1242

ccactcggtc ttgtactcgc acgatcgcgc gacgacggcg acgccgacgg cgactttcca 1302

gcgtcgctca acaggctggc tgtcgtcgcg ctcgctggtg cggctctcgt cgggtcggcg 1362

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<211> 262

<212> PRT

<213> Halobacterium salinarium

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Met Gly Leu Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser

35 40 45

Asp Pro Asp Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala

50 55 60

Ile Ala Phe Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr

65 70 75 80

Met Val Pro Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr

85 90 95

Ala Asp Trp Leu Phe Thr Thr Pro Leu Leu Leu Leu Asp Leu Ala Leu
 100 105 110

Leu Val Asp Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp
 115 120 125

Gly Ile Met Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr
 130 135 140

Ser Tyr Arg Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr
 145 150 155 160

Ile Leu Tyr Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met
 165 170 175

Arg Pro Glu Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val
 180 185 190

Val Leu Trp Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly
 195 200 205

Ala Gly Ile Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu
 210 215 220

Asp Val Ser Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg
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Ala Ile Phe Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly
 245 250 255

Ala Ala Ala Thr Ser Asp

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<212> DNA

<213> Artificial Sequence

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<210> 4

<211> 20

<212> DNA

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<223> Description of Artificial Sequence:oligonucleotide
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<210> 5

<211> 91

<212> DNA

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tcggcgacga cgcagaaggc ggagaaggag g 91

<210> 6

<211> 96

<212> DNA

<213> Artificial Sequence

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<400> 6

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<210> 7

<211> 26

<212> DNA

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<400> 7

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<210> 8

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide
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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide
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<400> 9

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<210> 10

<211> 15

<212> DNA

<213> Artificial Sequence

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<210> 11

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<212> DNA

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